

IN THE CLAIMS:

Please amend the following claims:

2. (Amended) A method according to claim 1, wherein the amounts of two nucleic acid sequences in a sample is compared by determining the PCR efficiencies of the two reactions [~~according to claim 1~~].

3. (Amended) A method according to [~~claims 1-2~~] claim 1, wherein the ratio of two nucleic acids in a test sample is determined using the relation:

$$\frac{N_{0A}}{N_{0B}} \propto \frac{(1 + \langle E_A \rangle)^{CT_A}}{(1 + \langle E_B \rangle)^{CT_B}}$$

where the CT values are measured in the test sample and the PCR efficiencies $\langle E \rangle$ are determined separately for a training set of representative samples comprising said nucleic acid sequence by the procedure in claim 1 or an equivalent procedure such as kinetic PCR.

4. (Amended) A method according to [~~claims 1-2~~] claim 1, wherein the ratio of two nucleic acid sequences is determined in a sample using the relation:

$$\frac{N_{0A}}{N_{0B}} = K_{RS} \frac{(1 + \langle E_A \rangle)^{CT_A}}{(1 + \langle E_B \rangle)^{CT_B}}$$

also taking into account the relative sensitivity of the two PCR assays.

5. (Amended) A method according to [~~claims 1-2~~], claim 1 wherein the amount of a nucleic acid sequence is determined in a biological sample [~~according to either of the claims 1-4~~] ; wherein the nucleic acid is RNA, preferably one or more mRNAs that have been converted to DNA by reverse transcription or a similar process.

6. (Amended) A method for diagnosing and/or classifying a disease by comparing the expression ratio of two genes by determining the ratio of the corresponding mRNAs in a sample according to [~~either of the claims 1-5~~] claim 1.

7. (Amended) A method according to claim 6, wherein lymphoma is diagnosed by comparing the expression of at least two genes [~~according to either of the claims 1-5~~], wherein the relative expression of the genes is different in clonal samples compared to healthy tissue.

11. (Amended) A method according to [~~claim 6-10~~] claim 6, wherein the degree of complementarity is at least 80%.

13. (Amended) A method according to [~~claim 1-6~~] claim 1, wherein CML is diagnosed by determining the expression of bcr-abl fusion transcript.

17. (Amended) A method for comparing the presence of splicing variants of a gene by determining their relative amounts according to [~~either of the claims 1-5~~] claim 1.

18. (Amended) A method for comparing the activities of alternative promoters by determining the relative amounts of their transcripts according to [~~either of the claims 1-5~~] claim 1.

19. (Amended) A method for determining the amount of virus or bacteria in a sample according to [~~either of the claims 1-5~~] claim 1.